

APPLICANT(S): CAPPOLA, Thomas. *et al.*
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AMENDMENTS TO THE CLAIMS

Please amend the claims as follows:

1-18. (Canceled).

19. (Withdrawn) A medium having disposed thereon a cRNA of *UQCRB*, *BTF3*, *ST13*, *CUL4A*, *TERF2IP*, *ARRB2*, *NPEPPS*, *ARRB2*, *NPEPPS*, *PIGB*, *APC*, *BCL7A*, *EDG4*, *IL17R*, *PGF*, *NFAT5*, *BIRC1*, *LILRB3*, *TM6SF2*, *CFLAR*, *SOD2*, *SLC16A3* or *SCD4*.

20. (Withdrawn) The medium of claim 19, wherein the medium is machine readable.

21. (Withdrawn) The medium of claim 20 in the form of a microarray chip.

22. (Withdrawn) The medium of claim 19, wherein the oligonucleotide is detectably labeled.

23. (Withdrawn) A kit for predicting transplant tolerance, said kit comprising a microarray comprising immobilized nucleic acids, wherein said nucleic acids exhibit complementarity to a *UQCRB*, *BTF3*, *ST13*, *CUL4A*, *TERF2IP*, *ARRB2*, *NPEPPS*, *ARRB2*, *NPEPPS*, *PIGB*, *APC*, *BCL7A*, *EDG4*, *IL17R*, *PGF*, *NFAT5*, *BIRC1*, *LILRB3*, *TM6SF2*, *CFLAR*, *SOD2*, *SLC16A3* and *SCD4* gene, or fragments thereof.

24. (Withdrawn) The kit of claim 23, further comprising immobilized nucleic acid whose sequence is complimentary to that set forth in SEQ ID Nos. 1 - 12.

25. (Withdrawn) The kit of claim 23, further comprising reagents for processing a biological sample and isolating mRNA from said sample.

26. (Withdrawn) The kit of claim 25, further comprising an agent which labels said mRNA isolated from said biological sample..
27. (Withdrawn) The kit of claim 23, further comprising instructions for use in determining the expression of said genes in a biological sample.
28. (Withdrawn) The kit of claim 27, further comprising directions for correlating said gene expression with a likelihood of transplant tolerance.
29. (Withdrawn) The kit of claim 23, wherein said kit further comprises a buffering agent, a preservative, or a protein stabilizing agent.
30. (Withdrawn) The kit of claim 23, wherein said kit further comprises an enzyme or a substrate.
31. (New) A method for identifying a cardiac transplant tissue rejection in a human subject, said method comprising:
 - determining a first gene expression profile in a blood sample taken from said human subject, wherein said first gene expression profile comprises the nucleic acid expression level of an ubiquinol-cytochrome c reductase binding protein (UQCRB); and
 - comparing said first gene expression profile to a pre-determined second gene expression profile, wherein said second gene expression profile comprises the nucleic acid expression level of UQCRB derived from blood samples collected from a human cardiac transplant population that does not have cardiac tissue rejection,
 - wherein a statistically significant increase in UQCRB expression in said first gene expression profile compared to said second gene expression profile is an indicative of cardiac transplant tissue rejection in said human subject.

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32. (New) The method of claim 31, wherein said first and second gene expression profiles further comprise the nucleic acid expression level of basic transcription factor 3 (BTF3), suppression of tumorigenicity 13 (ST13), and cullin 4A (CUL4A).
33. (New) The method of claim 32, wherein a statistically significant increase in BTF3, ST13, or CUL4 expression in said first gene expression profile compared to said second gene expression profile is an indicative of cardiac transplant tissue rejection in said human subject.
34. (New) The method of claim 31, wherein said first and second gene expression profiles further comprise the nucleic acid expression level of a CASP8 and FADD-like apoptosis regulator (CFLAR) gene.
35. (New) The method of claim 34, wherein a statistically significant decrease in CFLAR expression in said first gene expression profile compared to said second gene expression profile is an indicative of cardiac transplant tissue rejection in said human subject.
36. (New) The method of claim 31, wherein said first and second gene expression profiles comprise the expression of a plurality of expressed sequence tags (ESTs).
37. (New) The method of claim 36, wherein at least one of said expressed sequence tags comprises a nucleic acid sequence corresponding or homologous to SEQ ID. No.: 12.
38. (New) The method of claim 31, wherein said transplant is a cardiac allograft.
39. (New) The method of claim 31, wherein determining said first gene expression profile is conducted by the use of a microarray.